

University of Groningen

Classical Hodgkin lymphoma

Diepstra, Arjan

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Document Version

Publisher's PDF, also known as Version of record

Publication date:

2007

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):

Diepstra, A. (2007). *Classical Hodgkin lymphoma: population based studies on HLA and EBV*. [Thesis fully internal (DIV), University of Groningen]. [S.n.].

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Stellingen behorende bij het proefschrift

Classical Hodgkin lymphoma: population based studies on HLA and EBV

1. Classical Hodgkin lymphoma (cHL) is a heterogeneous disease.
2. Immune mechanisms, including antigen presentation, are intricately involved in the pathogenesis of cHL.
3. Functional studies in cHL are hampered by the scarcity of neoplastic cells, the lack of animal models and the limited representativity of cHL cell lines.
4. The Epstein Barr virus (EBV) is a versatile disease causing agent and can only be controlled by the human immune system.
5. Classical association analysis and the Haplotype Sharing Statistic can extract different information from a set of genotyping data.
6. Genotyping studies in complex diseases are more likely to identify pathogenetic pathways than to identify genetic mutations or polymorphisms relevant to general health care.
7. In individuals carrying the HLA-A*01 allele the increased susceptibility for developing cHL is virtually negligible.
8. Immunohistochemical analyses alone are not sufficient to study the function of the antigen presenting pathways.
9. Het belang dat over het algemeen aan de auteursvolgorde wordt gehecht, beïnvloedt de animo voor het opzetten van multidisciplinaire en internationale studies in negatieve zin.
10. Waar hard gewerkt wordt kan het niet (altijd) netjes zijn.
11. Spaak verkenning is 1 zee gen.
12. Met een fietscomputer en een MP3-spelertje kan de reistijd Paterswolde-UMCG met precies 5 minuten en 21 seconden verkort worden; dit kost wel ongeveer 10 minuten uitpuffen.

Arjan Diepstra, 7 november 2007